S. Gucker

RAW SEQUENCE LISTING DATE: 01/07/2002
PATENT APPLICATION: US/09/378,261 TIME: 14:39:31

#9

Input Set : N:\Crf3\RULE60\09378261.raw
Output Set: N:\CRF3\01072002\I378261.raw

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Fukudome, Kenji
Esmon, Charles T.

(ii) TITLE OF INVENTION: Cloning and Regulation of an Endothelial Cell Protein C/Activated Protein C Receptor

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Patrea L. Pabst
(B) STREET: 2800 One Atlantic Center, 1201 West Peachtree Street
(C) CITY: Atlanta
(D) STATE: Georgia
(E) COUNTRY: US
(F) ZIP: 30306-3450

ENTEREL

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
C--> **(A) APPLICATION NUMBER: US/09/378,261**
C--> **(B) FILING DATE: 20-Aug-1999**
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/289,699
(B) FILING DATE: 12-AUG-1994

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Pabst, Patrea L.
(B) REGISTRATION NUMBER: 31,284
(C) REFERENCE/DOCKET NUMBER: OMRF152

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (404)873-8794
(B) TELEFAX: (404)873-8795

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..1302
(D) OTHER INFORMATION: /note= "Nucleotides 25 through 738 encode the

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Endothelial Cell Protein Receptor of Sequence ID No. 2."
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
CAGGTCCGGA GCCTCAACTT CAGGATGTTG ACAACATTGC TGCCGATACT GCTGCTGTCT 60
GGCTGGGCCT TTTGTAGCCA AGACGCCTCA GATGGCCTCC AAAGACTTCA TATGCTCCAG 120
ATCTCCTACT TCCGCGACCC CTATCACGTG TGGTACCAGG GCAACGCGTC GCTGGGGGGA 180
CACCTAACGC ACGTGCTGGA AGGCCCAGAC ACCAACACCA CGATCATTCA GCTGCAGCCC 240
TTGCAGGAGC CCGAGAGCTG GGCGCGCACG CAGAGTGGCC TGCAGTCCTA CCTGCTCCAG 300
TTCCACGGCC TCGTGCGCCT GGTGCACCAG GAGCGGACCT TGGCCTTTCC TCTGACCATC 360
CGCTGCTTCC TGGGCTGTGA GCTGCCTCCC GAGGGCTCTA GAGCCCATGT CTTCTTCGAA 420
GTGGCTGTGA ATGGGAGCTC CTTTGTGAGT TTCCGGCCGG AGAGAGCCTT GTGGCAGGCA 480
GACACCCAGG TCACCTCCGG AGTGGTCACC TTCACCCTGC AGCAGCTCAA TGCCTACAAC 540
CGCACTCGGT ATGAACTGCG GGAATTCCTG GAGGACACCT GTGTGCAGTA TGTGCAGAAA 600
CATATTTCCG CGGAAAACAC GAAAGGGAGC CAAACAAGCC GCTCCTACAC TTCGCTGGTC 660
CTGGGCGTCC TGGTGGGCGG TTTCATCATT GCTGGTGTGG CTGTAGGCAT CTTCCTGTGC 720
ACAGGTGGAC GGCGATGTTA ATTACTCTCC AGCCCCGTCA GAAGGGGCTG GATTGATGGA 780
GGCTGGCAAG GGAAAGTTTC AGCTCACTGT GAAGCCAGAC TCCCCAACTG AAACACCAGA 840
AGGTTTGGAG TGACAGCTCC TTTCTTCTCC CACATCTGCC CACTGAAGAT TTGAGGGAGG 900
GGAGATGGAG AGGAGAGGTG GACAAAGTAC TTGGTTTGCT AAGAACCTAA GAACGTGTAT 960
GCTTTGCTGA ATTAGTCTGA TAAGTGAATG TTTATCTATC TTTGTGGAAA ACAGATAATG 1020
GAGTTGGGGC AGGAAGCCTA TGCGCCATCC TCCAAAGACA GACAGAATCA CCTGAGGCGT 1080
TCAAAAGATA TAACCAAATA AACAAGTCAT CCACAATCAA AATACAACAT TCAATACTTC 1140
CAGGTGTGTC AGACTTGGGA TGGGACGCTG ATATAATAGG GTAGAAAGAA GTAACACGAA 1200
GAAGTGGTGG AAATGTAAAA TCCAAGTCAT ATGGCAGTGA TCAATTATTA ATCAATTAAT 1260
AATATTAATA AATTTCTTAT ATTTAAAAAA AAAAAAAAAA AA 1302
(2) INFORMATION FOR SEQ ID NO: 2:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..365
(D) OTHER INFORMATION: /note= "Endothelial Cell Protein Receptor
encoded by
nucleotides 1 through 1302 of Sequence ID No. 1."
(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1..15
(D) OTHER INFORMATION: /note= "Amino acids 1-15 represent
a putative signal sequence."
(ix) FEATURE:
(A) NAME/KEY: Domain
(B) LOCATION: 211..236
(D) OTHER INFORMATION: /note= "Amino acids 211-236
represent a putative transmembrane domain."
(ix) FEATURE:
(A) NAME/KEY: Active-site

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(B) LOCATION: 47..174
(D) OTHER INFORMATION: /note= "Amino acids 47-49, 64-66, 136-138 and 172-174 represent potential N-glycosylation sites."
(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 17..186
(D) OTHER INFORMATION: /note= "Amino acids 17, 114, 118 and 186 represent extracellular cysteine residues."
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Leu Thr Thr Leu Leu Pro Ile Leu Leu Leu Ser Gly Trp Ala Phe
1               5                  10                  15
Cys Ser Gln Asp Ala Ser Asp Gly Leu Gln Arg Leu His Met Leu Gln
            20                  25                  30
Ile Ser Tyr Phe Arg Asp Pro Tyr His Val Trp Tyr Gln Gly Asn Ala
        35                  40                  45
Ser Leu Gly Gly His Leu Thr His Val Leu Glu Gly Pro Asp Thr Asn
    50                  55                  60
Thr Thr Ile Ile Gln Leu Gln Pro Leu Gln Glu Pro Glu Ser Trp Ala
65                  70                  75                  80
Arg Thr Gln Ser Gly Leu Gln Ser Tyr Leu Leu Gln Phe His Gly Leu
                85                  90                  95
Val Arg Leu Val His Gln Glu Arg Thr Leu Ala Phe Pro Leu Thr Ile
            100                 105                 110
Arg Cys Phe Leu Gly Cys Glu Leu Pro Pro Glu Gly Ser Arg Ala His
        115                 120                 125
Val Phe Phe Glu Val Ala Val Asn Gly Ser Ser Phe Val Ser Phe Arg
    130                 135                 140
Pro Glu Arg Ala Leu Trp Gln Ala Asp Thr Gln Val Thr Ser Gly Val
145                 150                 155                 160
Val Thr Phe Thr Leu Gln Gln Leu Asn Ala Tyr Asn Arg Thr Arg Tyr
                165                 170                 175
Glu Leu Arg Glu Phe Leu Glu Asp Thr Cys Val Gln Tyr Val Gln Lys
            180                 185                 190
His Ile Ser Ala Glu Asn Thr Lys Gly Ser Gln Thr Ser Arg Ser Tyr
        195                 200                 205
Thr Ser Leu Val Leu Gly Val Leu Val Gly Gly Phe Ile Ile Ala Gly
    210                 215                 220
Val Ala Val Gly Ile Phe Leu Cys Thr Gly Gly Arg Arg Cys
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO: 3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 244 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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Input Set : N:\Crf3\RULE60\09378261.raw
Output Set: N:\CRF3\01072002\I378261.raw

```
218      Met Leu Thr Lys Phe Leu Leu Leu Leu Leu Leu Leu Pro Gly Cys
219      1               5                   10                  15
221      Ala Phe Val Thr Pro Met Ala Pro Lys Ala Ala Tyr Ala Pro Asp Leu
222                  20                  25                  30
224      Leu Phe Pro Arg Pro Pro Ser Cys Glu Ala Ser Gly Gln Arg Ser Leu
225              35                  40                  45
227      Gly Lys Leu Leu Thr His Thr Leu Glu Gly Pro Ser Gln Asn Val Thr
228          50                  55                  60
230      Ile Leu Gln Leu Gln Pro Trp Gln Asp Pro Glu Ser Trp Glu Arg Thr
231      65                  70                  75                  80
233      Glu Ser Gly Leu Gln Ile Tyr Leu Thr Gln Phe Glu Ser Leu Val Lys
234                  85                  90                  95
236      Leu Val Tyr Arg Glu Arg Lys Glu Asn Val Phe Phe Pro Leu Thr Val
237                  100                 105                 110
239      Ser Cys Ser Leu Gly Cys Glu Leu Pro Glu Glu Glu Glu Glu Gly Ser
240              115                 120                 125
242      Glu Pro His Val Phe Phe Asp Val Ala Val Asn Gly Ser Ala Phe Val
243          130                 135                 140
245      Ser Phe Arg Pro Lys Thr Ala Val Trp Val Ser Gly Ser Gln Glu Pro
246      145                 150                 155                 160
248      Ser Lys Ala Ala Asn Phe Thr Leu Lys Gln Leu Asn Ala Tyr Asn Arg
249                  165                 170                 175
251      Thr Arg Tyr Glu Leu Gln Glu Phe Leu Gln Asp Thr Cys Val Glu Phe
252                  180                 185                 190
255      Leu Glu Asn His Ile Thr Thr Gln Asn Met Lys Gly Ser Gln Thr Gly
256              195                 200                 205
258      Arg Ser Tyr Thr Ser Leu Val Leu Gly Ile Leu Met Gly Cys Phe Ile
259          210                 215                 220
261      Ile Ala Gly Val Ala Val Gly Ile Phe Met Cys Thr Ser Gly Arg Gly
262      225                 230                 235                 240
264      Leu Leu Ile Ile
267  (2) INFORMATION FOR SEQ ID NO: 4:
269       (i) SEQUENCE CHARACTERISTICS:
270            (A) LENGTH: 335 amino acids
271            (B) TYPE: amino acid
272            (C) STRANDEDNESS: single
273            (D) TOPOLOGY: linear
275      (ii) MOLECULE TYPE: peptide
278      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
280       Met Gly Cys Leu Leu Phe Leu Leu Leu Trp Ala Leu Leu Gln Ala Trp
281       1               5                   10                  15
283       Gly Ser Ala Glu Val Pro Gln Arg Leu Phe Pro Leu Arg Cys Leu Gln
284                   20                  25                  30
286       Ile Ser Ser Phe Ala Asn Ser Ser Trp Thr Arg Thr Asp Gly Leu Ala
287               35                  40                  45
289       Trp Leu Gly Glu Leu Gln Thr His Ser Trp Ser Asn Asp Ser Asp Thr
290           50                  55                  60
292       Val Arg Ser Leu Lys Pro Trp Ser Gln Gly Thr Phe Ser Asp Gln Gln
293       65                  70                  75                  80
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```
295      Trp Glu Thr Leu Gln His Ile Phe Arg Val Tyr Arg Ser Ser Phe Thr
296                      85                  90                  95
298      Arg Asp Val Lys Glu Phe Ala Lys Met Leu Arg Leu Ser Tyr Pro Leu
299                  100                 105                 110
301      Glu Leu Gln Val Ser Ala Gly Cys Glu Val His Pro Gly Asn Ala Ser
302              115                 120                 125
304      Asn Asn Phe Phe His Val Ala Phe Gln Gly Lys Asp Ile Leu Ser Phe
305          130                 135                 140
307      Gln Gly Thr Ser Trp Glu Pro Thr Gln Glu Ala Pro Leu Trp Val Asn
308      145                 150                 155                 160
310      Leu Ala Ile Gln Val Leu Asn Gln Asp Lys Trp Thr Arg Glu Thr Val
311                      165                 170                 175
313      Gln Trp Leu Leu Asn Gly Thr Cys Pro Gln Phe Val Ser Gly Leu Leu
314                  180                 185                 190
317      Glu Ser Gly Lys Ser Glu Leu Lys Lys Gln Val Lys Pro Lys Ala Trp
318              195                 200                 205
320      Leu Ser Arg Gly Pro Ser Pro Gly Pro Gly Arg Leu Leu Leu Val Cys
321          210                 215                 220
323      His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Lys Trp Met Arg
324      225                 230                 235                 240
326      Gly Glu Gln Glu Gln Gln Gly Thr Gln Pro Gly Asp Ile Leu Pro Asn
327                      245                 250                 255
329      Ala Asp Glu Thr Trp Tyr Leu Arg Ala Thr Leu Asp Val Val Ala Gly
330                  260                 265                 270
332      Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser Ser Leu Glu Gly
333              275                 280                 285
335      Gln Asp Ile Val Leu Tyr Trp Gly Gly Ser Tyr Thr Ser Met Gly Leu
336          290                 295                 300
338      Ile Ala Leu Ala Val Leu Ala Cys Leu Leu Phe Leu Leu Ile Val Gly
339      305                 310                 315                 320
341      Phe Thr Ser Arg Phe Lys Arg Gln Thr Ser Tyr Gln Gly Val Leu
342                      325                 330                 335
344  (2) INFORMATION FOR SEQ ID NO: 5:
346       (i) SEQUENCE CHARACTERISTICS:
347            (A) LENGTH: 336 amino acids
348            (B) TYPE: amino acid
349            (C) STRANDEDNESS: single
350            (D) TOPOLOGY: linear
352      (ii) MOLECULE TYPE: peptide
355      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
357       Met Arg Tyr Leu Pro Cys Leu Leu Leu Trp Ala Phe Leu Gln Val Trp
358       1               5                   10                  15
360       Gly Gln Ser Glu Val Gln Gln Lys Asn Tyr Thr Phe Arg Cys Leu Gln
361                   20                  25                  30
363       Thr Ser Ser Phe Ala Asn Ile Ser Trp Ser Arg Thr Asp Ser Leu Ile
364               35                  40                  45
366       Leu Leu Gly Asp Leu Gln Thr His Arg Trp Ser Asn Asp Ser Ala Thr
367           50                  55                  60
369       Ile Ser Phe Thr Lys Pro Trp Ser Gln Gly Lys Leu Ser Asn Gln Gln
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VERIFICATION SUMMARY DATE: 01/07/2002
PATENT APPLICATION: US/09/378,261 TIME: 14:39:32

Input Set : N:\Crf3\RULE60\09378261.raw
Output Set: N:\CRF3\01072002\I378261.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]